MergeToCure: a New Strategy to Allocate Cure in an Epidemic over a Grid-like network Using a Scale-Free Abstraction

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MergeToCure: a New Strategy to Allocate Cure in an Epidemic over a Grid-like network Using a Scale-Free Abstraction [⋆]

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Abstract: In the context of epidemic spreading over a network the problem of allocating a limited number of cure to curb the spreading is often discussed. While strategies exist for heterogeneous networks as scale-free networks (networks with a power-law degree distribution), we introduce here a new strategy for homogeneous networks as grid-like networks. To do so we use a scale-free abstraction of the network allowing to identify the most interesting zones to cure. Moreover we present a theoretical result linking the scale-free coefficient and the efficiency of the strategy of allocation in scale-free networks.

Keywords: Scale-free network, Epidemic spreading, Grid network, Network reliability.

1. INTRODUCTION

The mathematical modelling of epidemic spreading aims to evaluate the progression of an epidemic through a population and to design tools to control the propagation. A large class of the approaches belongs to the compartmental models in which the population is divided in distinct compartments describing the state of each individual. In Kermack and McKendrick (1932), the initial work on this subject, the individuals are divided in three categorises: Susceptible, Infected, and Recovered, interacting between them. Afterwards, to get closer to the reality, other models proposed to consider several other compartments. While it uses only two compartments, the SIS (Susceptible-Infected-Susceptible) model is often used. It is this model which is considered within this article. For the dynamical system community the SIR and SIS model applied on grid network are very close to cellular automaton models called respectively forest-fire model (Bak et al. (1990)) and contact process model (Harris (1974)). The mathematical modelling of epidemic spreading has known a new interest in recent years, as they are now used within the framework of network theory, allowing to take into account the connections between individuals among the population. A new class of models emerged then.

Although we use in this article the terminology of epidemics, let us note that these models are also used in other contexts such as: spreading of computer viruses over web networks (e.g. Balthrop et al. (2004)) or information spreading over social networks (e.g. Leskovec et al. (2007)). Within the frame of network theory a common problem is the allocation of a limited number of cure within a population. As cured individuals can not be infected or infect other individuals they can be considered as removed from the network. In Dezső and Barabási (2002), the problem is treated in the context of scale-free networks. It is shown that, for this type of networks, assigning cures to the highest connected nodes curbs efficiently the spreading. However, there is no result linking the scale-free coefficient (i.e. the coefficient of the power-law) to the efficiency of this strategy. Moreover, in homogeneous network such as grid-like network, the absence of hubs prevents the efficiency of this strategy. Although they used a slightly different model, also Rhodes and Anderson (1997) poses the question of assigning cure in a grid network. The strategy proposed requires to know the location of the seed of the epidemic, which is often impossible in real cases.

The main contributions of this paper are i) the link established between the scale-free coefficient and the efficiency of the hub-removal strategy in scale-free networks and ii) the introduction of a strategy to allocate cures in a grid-like network. The approach consists in finding zones-hubs according to a scale-free abstraction of the homogeneous network. These zones are then removed from the network to avoid the epidemic to spread through them. We show numerically that this strategy is better than other strategies for a same number of cures and for a large range of the parameters.

In section II, we introduce more precisely the model and we describe the problem and previous results. Within this section we show how the scale-free coefficient influences the efficiency of the hub-removal strategy in scale-free networks. In section III, we present an algorithm allowing to find a scale-free abstraction out of an homogeneous network. The main results are presented in section IV in which we describe the cure allocation strategy and experimental results.

2. PROBLEM INTRODUCTION

2.1 Preliminaries

In this section we give some graph-theoretical definitions allowing to define properly scale-free graphs. Note that, within this work, we talk about graph or network without any distinction.

Consider a directed graph G, represented by the triple $(\mathcal{A}, \mathcal{V}, \mathcal{E})$ where $\mathcal{A}$ is the adjacency matrix, whose non-zeros values indicate edges: $\mathcal{A}_{i,j} = 1$ means that there is an edge $i \longrightarrow j$. $\mathcal{V}$ is the set of vertices and $\mathcal{E}$ the set of edges. In a graph G, we call degree of a node the number of connection that it has. We denote Π_G the degree distribution of G, i.e.

$$\Pi_G(k) = \frac{|v \in \mathcal{V}, \deg(v) = k|}{|\mathcal{V}|}$$

where $\deg(v)$ is the degree [1] of the node v and $|\mathcal{S}|$ gives the cardinal of the set $\mathcal{S}$. We give now a definition of scale-free graph:

Definition (scale-free graph): A graph is scale-free if its degree distribution is proportional to a power law:

$$\Pi_G(k) \propto k^{-\alpha}, \qquad (1)$$

where $\alpha > 0$ is called the scale-free coefficient. In practice we call scale-free graph any graph whose degree distribution is *relatively* close to a power law.

2.2 The SIS model: original form and network form

Let now introduce the SIS (Susceptible-Infected-Susceptible) model used to study epidemic spreading. In this model, each individual within the population can be either susceptible (sound) or infected. An infected individual recovers at a rate γ, and a susceptible individual is infected at a rate $i\nu$, where i is the proportion of infected individuals within the population as illustrated in Fig. 1. In this model, the evolution of the number of infected individuals I and the number of susceptible individuals S is described by the following differential equations :

$$\frac{dI}{dt} = -\gamma I + i\nu S \qquad (2)$$

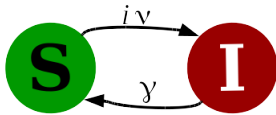$$\frac{dS}{dt} = \gamma I - i\nu S \qquad (3)$$

Fig. 1. Illustration of the exchanges between susceptible and infected compartments in the SIS model.

As said in the introduction, this model does not take into account the interconnections inside the population. Yet, one can imagine that in a population where individuals are highly-connected a disease will spread more quickly than in a poorly-connected population. Thus the SIS model has been adapted to networks.

[1] as we consider directed graphs, the degree can be either in-degree or out-degree. As the computations and the results remain the same for both cases, the degree used is not precised

In its network version, the evolution is in discrete time and at each time step an infected individual recovers with a probability γ, and a susceptible individual is infected with a probability ν, if and only if it is connected to at least one infected individual. In the following we denote $x = (x_1, \cdots, x_N)$ the population and we have $x_i = 1$ if the i-th individual is infected and $x_i = 0$ if it is susceptible, we denote also $\mathcal{N}_i$ the set of neighbours of the node i . We have then:

$$\begin{cases} \mathbb{P}(x_i(k+1) = 1 | x_i(k) = 0) = \nu & \text{if } \exists j \in \mathcal{N}_i, \ x_j(k) = 1 \\ \mathbb{P}(x_i(k+1) = 1 | x_i(k) = 0) = 0 & \text{if } \forall j \in \mathcal{N}_i, \ x_j(k) = 0 \\ \mathbb{P}(x_i(k+1) = 0 | x_i(k) = 1) = \gamma \end{cases}$$

$$(4)$$

Model (4) has been used for example in Dezső and Barabási (2002) and Pastor-Satorras and Vespignani (2001). After few steps, the system stabilises in a steady state with a proportion of infected nodes fluctuating around an average called the prevalence. Let's note that the prevalence, denoted ρ, only depends on the graph G and the infection rate $\lambda = \frac{\nu}{\gamma}$, but not on the initial subset of infected nodes (as long as this one is non-empty). We will then note $\rho(G, \lambda)$.

2.3 Allocating cure as a minimisation problem

As presented in Nowzari et al. (2016), one of the main challenges in the modelling of epidemic is to control it in view to reduce the spread of the disease. One of the tools which can be used to control an epidemic is curing individuals. In this case, the cured individuals can be considered as nodes removed from the network as they can not be infected or infect other individuals. In this perspective, the cure can also be viewed as a vaccination or a quarantine. We consider that the cure is given before the beginning of the epidemic.

If it is possible financially and logistically to cure all individuals, then the epidemic will not spread at all. However an interesting problem is posed when the number of cures is limited: What is the most efficient allocation of the cure to reduce the prevalence? Mathematically, this problem can be posed as follow: Giving a graph G and a number of cure m, find a subset of nodes Γ of size m solution of:

$$\min_{|\Gamma|=m} \rho(G_{\bar{\Gamma}}, \lambda) \qquad (5)$$

where $\bar{\Gamma}$ is the complementary set of Γ and $G_{\bar{\Gamma}}$ is the graph obtained by considering only the nodes in $\bar{\Gamma}$ and the edges between them. Intuitively, the best choice is to remove nodes such that the network becomes less connected and so the epidemic can not spread easily.

However, the node removal problem is NP-complete as shown in Van Mieghem et al. (2011). Thus several papers propose heuristics to approximately solve this problem. Essentially it is proposed to remove the most important nodes. Holme et al. (2002) proposes to remove nodes with the highest betweenness centrality, Miller and Hyman (2007) the highest PageRank and Dezső and Barabási (2002) the highest degree. This last approach is particularly efficient in scale-free networks as shown in the next section.

2.4 Allocating cures in scale-free networks

We see now some results about the spreading of the epidemic and a cure allocation strategy in scale-free networks. Anderson et al. (1992) shows that in a grid or a random network it exists an epidemic threshold λ_c under which the prevalence is always zero:

$$\forall \lambda < \lambda_c, \quad \rho(G_{hom}, \lambda) = 0 \qquad (6)$$

where G_{hom} is any *homogeneous* network (grid or random). Moreover, the threshold λ_c is proportional to the inverse of the variance of the degree distribution of the graph as:

$$\lambda_c = \frac{<k>}{<k^2>} \qquad (7)$$

In a scale-free network with $\alpha < 3$, when the number of nodes goes to infinity the variance of the degree distribution tends to infinity and then the epidemic threshold becomes null. Thus, in scale-free networks, even with an infection rate arbitrarily small, the epidemic will persist. However, Dezső and Barabási (2002) shows that it is possible to restore such an epidemic threshold by removing the biggest hubs, and this threshold can even be made larger than in a homogeneous network by removing enough hubs. Precisely, if we consider a scale-free network build with the Barabasi-Albert model, we have:

$$\lambda_c = \frac{k_0 - m}{k_0 m} \ln^{-1}\left(\frac{k_0}{m}\right) \qquad (8)$$

where m is the number of edges added at each step in the B.-A. model and k_0 is the degree above witch every nodes is removed. We present here a proposition on the influence of the scale-free coefficient on the threshold in the frame of the hub-removal strategy:

Theorem 1. Consider an infinite-size network with a perfect scale-free degree distribution with a coefficient α. Let $\lambda_c(\alpha, \tau)$ be the prevalence obtained when a proportion $\tau \in [0; 1]$ of the highest connected nodes is removed from the network. For every $h > 0$, we have:

$$\lambda_c(\alpha + h, \tau) > \lambda_c(\alpha, \tau) \qquad (9)$$

Thus, the higher α, the higher is the threshold and so the more efficient is the strategy.

Proof. Let us consider a scale-free network with an infinite size and a coefficient α. Let us remove a proportion $\tau \in [0; 1]$ of the highest connected nodes. Thanks to (8), we have:

$$\lambda_c(\alpha, \tau) = \frac{K(\alpha, \tau) - m}{K(\alpha, \tau)m} \ln^{-1}\left(\frac{K(\alpha, \tau)}{m}\right) \qquad (10)$$

where $K(\alpha, \tau)$ is the degree such that a proportion of τ nodes has a degree larger than $K(\alpha, \tau)$. We know that $K(\alpha, \tau)$ is linked with τ and α by the Riemann zeta function ζ as:

$$\frac{H_{K(\alpha,\tau),\alpha}}{\zeta(\alpha)} = 1 - \tau, \qquad (11)$$

where $H_{k,\alpha}$ is the generalised harmonic number $H_{k,\alpha} = \sum_{i=1}^{k} i^{-\alpha}$. It is clear that $H_{k,\alpha}$ increases with k. By computing the derivative, it is also possible to show that $\frac{H_{k,\alpha}}{\zeta(\alpha)}$ increases with α. Thus, if τ is fixed, then $K(\alpha, \tau)$ decreases when α increases. Moreover λ_c decreases with $K(\alpha, \tau)$. Thus, λ_c increases with α. $\square$

To capture the prevalence of the epidemic in a scale-free network, it is useful to decompose it as follows:

$$\rho = \sum_{k=1}^{+\infty} \Pi(k)\rho_k \qquad (12)$$

Thanks to Pastor-Satorras and Vespignani (2001), with a mean-field approximation, we have:

$$\rho_k = \frac{kg_\lambda}{1 + kg_\lambda} \qquad (13)$$

Where g_λ is positive and depends only on the infection rate. However, there is no result on the evolution of this prevalence when hubs are removed. We present here a proposition on the influence of the scale-free coefficient on the prevalence of the epidemic:

Theorem 2. Consider an infinite-size network with a perfect scale-free degree distribution with a coefficient α. Let $\rho(\alpha, \tau)$ be the prevalence obtained when a proportion $\tau \in [0; 1]$ of the highest connected nodes is removed from the network. For every $h > 0$, we have:

$$\rho(\alpha + h, \tau) < \rho(\alpha, \tau) \qquad (14)$$

Thus, the higher α, the lower is the threshold and so the more efficient is the strategy.

Proof. Considering the same notations as before, we have:

$$\rho = \sum_{k=1}^{+\infty} \Pi(k)\rho_k \qquad (15)$$

Now if we denote $\rho(\alpha, \tau)$ the prevalence after removing a proportion τ of the highest connected nodes in an α-scale-free graph, we have:

$$\rho(\alpha, \tau) = \sum_{k=1}^{K(\alpha,\tau)} \Pi(k)\rho_k \qquad (16)$$

Let us remark that in (16) we should replace ρ_k with $\rho_{k'}$ with $k' < k$. Indeed, the removal of hubs makes the degree of remaining nodes lower. However, in the limit of infinite-size graph we consider this as negligible which is verified numerically.
By developing (16) we find:

$$\rho(\alpha, \tau) = \sum_{k=1}^{K(\alpha,\tau)} \frac{k^{1-\alpha}g_\lambda}{1 + kg_\lambda} \qquad (17)$$

and, reminding that $K(\alpha, \tau)$ decreases with α, it follows that, $\forall h > 0$:

$$\rho(\alpha + h, \tau) - \rho(\alpha, \tau) =$$
$$\sum_{k=1}^{K(\alpha+h,\tau)} \frac{k^{1-(\alpha+h)}g_\lambda}{1 + kg_\lambda} - \sum_{k=1}^{K(\alpha,\tau)} \frac{k^{1-\alpha}g_\lambda}{1 + kg_\lambda}$$

Now as k^x increases with x, the terms in the first sum are smaller than the terms in the second sum. Moreover the first sum has less terms. Thus, the first sum is smaller than the second sum and so have proved (14). $\square$

With these two results we have shown that for the hub-removal strategy in a scale-free network, the best results are obtained with a large α. This result can be interpreted as follow: with a large α the hubs are highly connected, and so their removal cuts a lot of connections in the network.

However this strategy is efficient if the network has a complex structure in which highly-connected nodes emerge naturally. If the initial network is homogeneous this strategy can not be applied. In the same way, the strategies recommending to remove nodes with the highest PageRank or the highest betweenness centrality lose their interest in an homogeneous network.

Nevertheless, it appears interesting to find a scale-free abstraction of an arbitrary network in view to highlight some zone-hubs which are more interesting to cure. To find this scale-free abstraction we use the algorithm Merge-ToScaleFree described in the next section.

3. MERGE TO SCALE-FREE

Martin et al. (2018) presents an algorithm allowing to find a scale-free abstraction out of an arbitrary network in view to benefit of the scale-free properties [2]. The aim of this algorithm is to find a partition of the original network resulting in a scale-free network. Besides the scale-freeness of the output network, this algorithm allows to preserve some properties of the initial network, such as the eigenvector centrality. In this paper, we will not focus on the preservation of these properties but only on the scale-free structure of the abstracting network. For our purpose the algorithm can be described as follows:

(1) Consider an initial graph $G_0 = (\mathcal{A}, \mathcal{V}, \mathcal{E}) \in \Gamma$.
(2) A random small subset of edges $\tilde{\mathcal{E}}$ is generated.
(3) For each edge $(v, w) \in \tilde{\mathcal{E}}$, a new graph $G_{(v,w)}$ is computed. The graph $G_{(v,w)}$ is similar to the graph G but with the nodes v and w merged into one single node.
(4) Among all the graphs generated, the one whose degree distribution is the closest to a power-law with a given coefficient α is retained and the algorithm restarts in (2).
(5) The algorithm is stopped when the scale-freeness of the current graph can not be improved anymore.

Let's remark that only a random subset of edges is tested instead of the whole set of edges. This allows to reduce considerably the complexity of the algorithm and it is shown numerically that there is no major impact on the scale-freeness of the outputting graph as soon as the subset is larger to an empirical threshold.

Since nodes in the final graph originate from merging nodes of the initial graph, the algorithm produces a partition of the initial graph. In this partition, each region corresponds to a node in the scale-free abstraction. In order to curb the spreading of the epidemic, it seems interesting to protect the regions corresponding to hubs. The next section presents in detail this strategy.

4. THE STRATEGY MERGE TO CURE

4.1 Description of the strategy

The idea of the strategy is to emphasise zones which play the role of hubs within the network, thanks to the

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[2] A detailed description of the algorithm and its motivation is available in Martin et al. (2018) and in video at *https://www.youtube.com/watch?v=UXc76Z5Ek3M*

algorithm MergeToScaleFree, and to focus on curing these zones. The strategy can be detailed as follows:

(1) Extract a scale-free abstraction out of the original homogeneous network.
(2) Identify the hubs in the scale-free abstraction, corresponding to zones-hubs in the initial network.
(3) Assign a cure to the nodes at the border of the zone-hubs.

The interest of the removal of hub in a scale-free network is to cut the communication between some nodes in the network. Then, in the case of zones-hubs, it is sufficient to only remove the border of these zones. Figure 4 provides an illustration of the strategy.

Remark on the relation with meta-population models It is possible to establish a parallel between this idea and the meta-population models. In these models, introduced in Bailey (1986), nodes does not represent individuals but groups of individuals such as cities. In our case, if the initial network is a network of individual at the scale of a country for example. Our strategy consists in finding how to regroup these individuals at a coarser scale, as cities, and so find a meta-population abstraction of the initial model. Then we focus on how to curb the epidemic in the meta-population network. As the meta-population network is designed to be scale-free then we identify which cities are the most interesting to protect in view to reduce the spreading of the epidemic.

4.2 Experimental results

In this section, we present the experimental set up to validate our strategy. We first describe how the experiment has been set, then we present the main results.

The grid-like networks Grid networks or lattice networks are a family of networks consisting in simply a grid of size $N \times N$ in which each of the N^2 intersections is a node. In our case, in view to get more realistic networks we add some random irregularities: some nodes are removed, some shortcuts are created and some edges are unidirectional. This is what we call grid-like networks. Figure 3 presents an example from this family of networks.

Experiments To test the efficiency of our method we will proceed as follow: Considering an initial grid network G we will numerically compute its prevalence, thanks to (4), after removing nodes according to different strategies:

(1) MergeToCure: curing the nodes at the border of the N_{hub} highest connected node in the scale-free abstraction. We denote n_{cure} the number of nodes hence removed.
(2) By curing randomly n_{cure} nodes
(3) By curing the n_{cure} nodes with the highest degree.
(4) By curing the n_{cure} nodes with the highest betweenness centrality.
(5) By curing the n_{cure} nodes with the highest PageRank.

All these strategies are compared with the null case where no cure is assigned in the network. For each strategy σ we compute the benefit B_σ as:

$$B_\sigma(n_{cure}, \lambda) = \frac{\rho(G_{\bar{\Gamma}(\sigma, n_{cure})}, \lambda) - \rho(G, \lambda)}{\rho(G, \lambda)} \quad (18)$$

(a) The initial grid-like network.

(b) The partition of the network obtained with the algorithm MergeToScaleFree.

(c) The scale-free network abstracting the initial grid-like network.

(d) Removal of the hubs

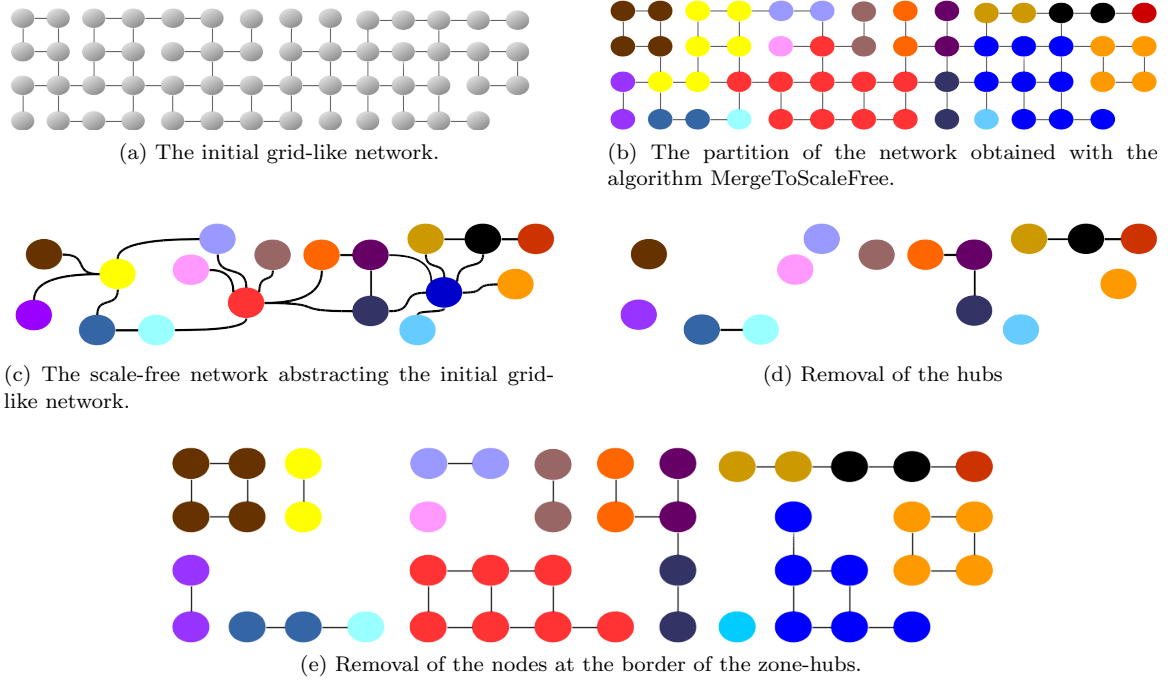(e) Removal of the nodes at the border of the zone-hubs.

Fig. 2. Illustration of the strategy MergeToCure to find a subset of nodes to cure in a grid-like network. For simplicity, we represent here an undirected network, but the same process can be applied to a directed network.
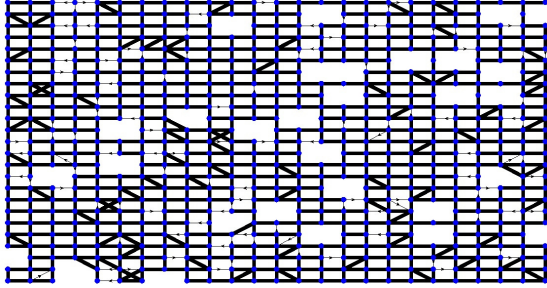

Fig. 3. Example of a grid-like network 25×25. Thicker edges represents double-way edges.

which corresponds to the benefit brought by the cure allocation strategy σ with respect to the case with no cure allocated.

Results   In the simulation presented in Fig. 4, a tenth of the population is infected at the initial time. The experiments are done with $N_{hub} = \{1; 2; 3; 4\}$ and the percentage of nodes hence removed is precised for each result. The abstracting scale-free is generated with a scale-free coefficient $\alpha = 2.8$ which is rather large for a scale-free network (usually $\alpha \in [2; 3]$). The value of the infection rate λ is varying between 0.4 and 4 with a step of 0.1. The results are averaged over 50 realisations with a different set of initially infected nodes. The network considered is a 60×60 grid-like network which contains then 3287 nodes.

We observe that the MergeToCure strategy has a larger benefit than all other strategies when $\lambda \gtrsim 1$ and $n_{cure} \lesssim 25\%$. For a large proportion of nodes removed (larger than 30% of the population) the hub strategy becomes more efficient than the MergeToCure strategy. We claim then, that, in a grid network, the MergeToCure strategy is more efficient to reduce the prevalence than other strategies for

parameters: $(\lambda, n_{cure}) \in]1; +\infty[\times]0; 0.3N]$, where N is the number of nodes in the network. To have an idea of the value of λ for real disease, Eames and Keeling (2002), for example, estimates this value for sexually transmissible disease between $[0.76; 1.52]$. Thus, MergeToCure is efficient for rather infectious disease.

Influence of the scale-free coefficient   Theorem 1 and theorem 2 hold in the framework of the hub-removal strategy in a perfectly scale-free network of infinite size. To figure out how these results impact the MergeToCure strategy on finite-size networks we made some simulations similar to the simulations presented before. In this case we only focus on the results about the prevalence and not on the threshold. Thus, we consider the benefit $B(n_{cure}, \lambda, \alpha)$ with $n_{cure} = 25\%$ and varying λ and α. Figure 5 shows the results. As expected, the benefit tends to be higher for high value of α.

5. CONCLUSION

In the context of epidemic spreading over a network, the question of assigning a limited number of cure to limit the epidemic spreading is often posed. A classical result claims that in a scale-free network an efficient strategy consists in curing the highly connected nodes. We show theoretically that the higher is the scale-free coefficient the more efficient is the strategy. Based on these results, we propose a strategy of cure allocation for homogeneous network. We show numerically that this strategy is better than all other strategies for a large range of parameters. While the numerical tests show satisfying results, this article raise some other questions which seem interesting to explore: Is our approach extensible to other epidemic model as SIR? How this strategy would be applicable to a practical case such as computer grid network? Let us remark finally that the idea of using an
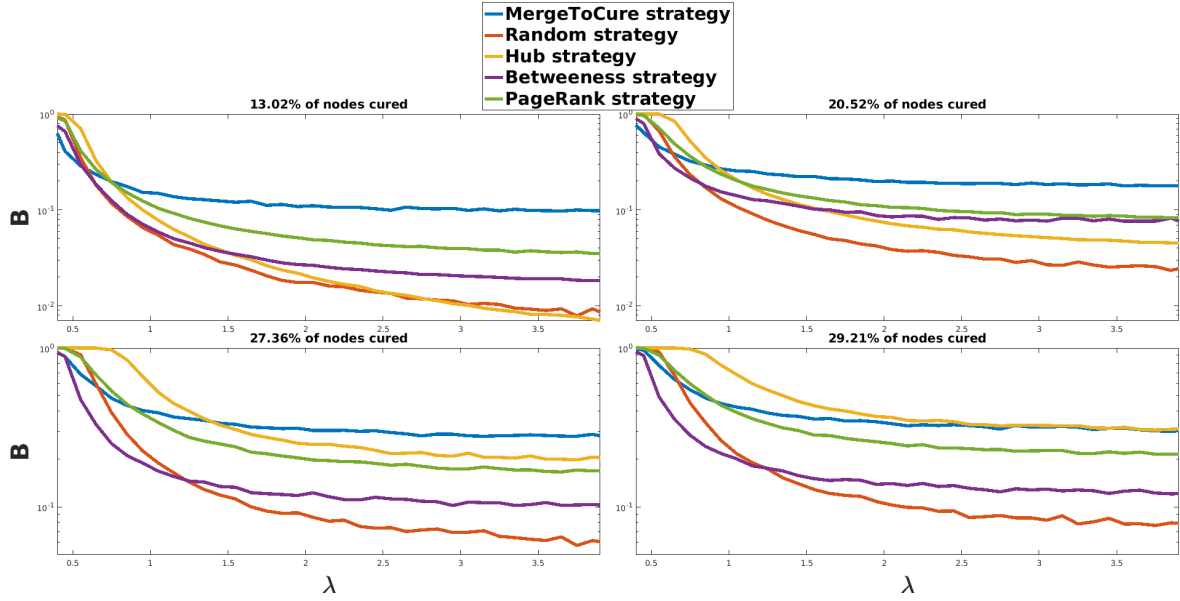
Fig. 4. Averaged benefit brought by each strategy for different value of λ and N_{hub} in a 60×60 grid network.
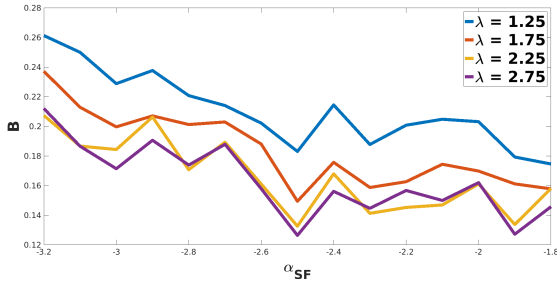

Fig. 5. Benefit brought by the strategy MergeToCure in function of the scale-free coefficient of the abstracting network.

abstraction to identify zones to cure may also be applied with betweenness centrality or PageRank centrality. In this case, it would be necessary to have an algorithm to find an abstracting network having nodes with a large centrality.

REFERENCES

Anderson, R.M., May, R.M., and Anderson, B. (1992). *Infectious diseases of humans: dynamics and control*, volume 28. Wiley Online Library.

Bailey, N.T. (1986). Macro-modelling and prediction of epidemic spread at community level. *Mathematical Modelling*, 7(5-8), 689–717.

Bak, P., Chen, K., and Tang, C. (1990). A forest-fire model and some thoughts on turbulence. *Physics letters A*, 147(5-6), 297–300.

Balthrop, J., Forrest, S., Newman, M.E., and Williamson, M.M. (2004). Technological networks and the spread of computer viruses. *Science*, 304(5670), 527–529.

Dezső, Z. and Barabási, A.L. (2002). Halting viruses in scale-free networks. *Physical Review E*, 65(5), 055103.

Eames, K.T. and Keeling, M.J. (2002). Modeling dynamic and network heterogeneities in the spread of sexually transmitted diseases. *Proceedings of the National Academy of Sciences*, 99(20), 13330–13335.

Harris, T.E. (1974). Contact interactions on a lattice. *The Annals of Probability*, 969–988.

Holme, P., Kim, B.J., Yoon, C.N., and Han, S.K. (2002). Attack vulnerability of complex networks. *Physical review E*, 65(5), 056109.

Kermack, W.O. and McKendrick, A.G. (1932). Contributions to the mathematical theory of epidemics. ii.the problem of endemicity. *Proc. R. Soc. Lond. A*, 138(834), 55–83.

Leskovec, J., McGlohon, M., Faloutsos, C., Glance, N., and Hurst, M. (2007). Patterns of cascading behavior in large blog graphs. In *Proceedings of the 2007 SIAM international conference on data mining*, 551–556. SIAM.

Martin, N., Frasca, P., and Canudas-De-Wit, C. (2018). A network reduction method inducing scale-free degree distribution. In *ECC 2018 - European Control Conference*, 1–6. Limassol, Cyprus. URL https://hal.archives-ouvertes.fr/hal-01769015.

Miller, J.C. and Hyman, J.M. (2007). Effective vaccination strategies for realistic social networks. *Physica A: Statistical Mechanics and its Applications*, 386(2), 780–785.

Nowzari, C., Preciado, V.M., and Pappas, G.J. (2016). Analysis and control of epidemics: A survey of spreading processes on complex networks. *IEEE Control Systems*, 36(1), 26–46.

Pastor-Satorras, R. and Vespignani, A. (2001). Epidemic spreading in scale-free networks. *Physical review letters*, 86(14), 3200.

Rhodes, C. and Anderson, R.M. (1997). Epidemic thresholds and vaccination in a lattice model of disease spread. *Theoretical Population Biology*, 52(2), 101–118.

Van Mieghem, P., Stevanović, D., Kuipers, F., Li, C., Van De Bovenkamp, R., Liu, D., and Wang, H. (2011). Decreasing the spectral radius of a graph by link removals. *Physical Review E*, 84(1), 016101.